

TQ
RAW SEQUENCE LISTING
PATENT APPLICATION US/09/340,690OIPE #4
DATE: 07/12/1999
TIME: 15:34:13

INPUT SET: S32510.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Ni, Jian
6 Rosen, Craig A.
7 Gentz, Reiner L.
8 Lyn, Sally Doreen Patricia
9 Hurle, Mark Robert
10
11 (ii) TITLE OF INVENTION: Human Tumor Necrosis Factor
12 Receptor-Like 2
13
14 (iii) NUMBER OF SEQUENCES: 26
15
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
18 (B) STREET: 1100 New York Ave, Suite 600
19 (C) CITY: Washington
20 (D) STATE: DC
21 (E) COUNTRY: USA
22 (F) ZIP: 20005-3934
23
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER:
32 (B) FILING DATE:
33 (C) CLASSIFICATION:
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: US 08/464,595
37 (B) FILING DATE: 05-JUN-1995
38
39 (vii) PRIOR APPLICATION DATA:
40 (A) APPLICATION NUMBER: US 08/741,095
41 (B) FILING DATE: 30-OCT-1996
42
43 (vii) PRIOR APPLICATION DATA:
44 (A) APPLICATION NUMBER: US 08/462,962
45 (B) FILING DATE: 05-JUN-1995
46

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AUG 12 1999
TC 1600 MAIL ROOM

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PATENT APPLICATION US/09/340,690DATE: 07/12/1999
TIME: 15:34:13

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47 (vii) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: US 08/462,315
49 (B) FILING DATE: 05-JUN-1995
50
51 (vii) PRIOR APPLICATION DATA:
52 (A) APPLICATION NUMBER: WO PCT/US95/05058
53 (B) FILING DATE: 27-APR-1995
54
55 (viii) ATTORNEY/AGENT INFORMATION:
56 (A) NAME: Steffe, Eric K.
57 (B) REGISTRATION NUMBER: 36,688
58 (C) REFERENCE/DOCKET NUMBER: 1488.0770007/EKS/SGW
59
60 (ix) TELECOMMUNICATION INFORMATION:
61 (A) TELEPHONE: 202-271-2600
62 (B) TELEFAX: 202-271-2540
63
64

65 (2) INFORMATION FOR SEQ ID NO:1:
66
67 (i) SEQUENCE CHARACTERISTICS:
68 (A) LENGTH: 1704 base pairs
69 (B) TYPE: nucleic acid
70 (C) STRANDEDNESS: double
71 (D) TOPOLOGY: linear
72
73 (ii) MOLECULE TYPE: DNA (genomic)
74
75
76 (ix) FEATURE:
77 (A) NAME/KEY: CDS
78 (B) LOCATION: 265..1113
79
80 (ix) FEATURE:
81 (A) NAME/KEY: sig_peptide
82 (B) LOCATION: 265..372
83
84 (ix) FEATURE:
85 (A) NAME/KEY: mat_peptide
86 (B) LOCATION: 373..1113
87
88

89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
90

91	GCACGAGCTG CCTCCCGCAG GCGCCACCTG TGTCCCCCAG CGCCGCTCCA CCCAGCAGGC	60
92		
93	CTGAGCCCCT CTCTGCTGCC AGACACCCCC TGCTGCCCAC TCTCCTGCTG CTCGGGTTCT	120
94		
95	GAGGCACAGC TTGTCACACC GAGGCGGATT CTCTTTCTCT TTCTCTTTCT CTTCTGGCCC	180
96		
97	ACAGCCGCAG CAATGGCGCT GAGTTCCTCT GCTGGAGTTC ATCCTGCTAG CTGGGTTCCC	240
98		
99	GAGCTGCCGG TCTGAGCCTG AGGC ATG GAG CCT CCT GGA GAC TGG GGG CCT	291

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100		Met	Glu	Pro	Pro	Gly	Asp	Trp	Gly	Pro										
101		-36	-35					-30												
102																				
103	CCT	CCC	TGG	AGA	TCC	ACC	CCC	AAA	ACC	GAC	GTC	TTG	AGG	CTG	GTG	CTG				339
104	Pro	Pro	Trp	Arg	Ser	Thr	Pro	Lys	Thr	Asp	Val	Leu	Arg	Leu	Val	Leu				
105			-25					-20					-15							
106																				
107	TAT	CTC	ACC	TTC	CTG	GGA	GCC	CCC	TGC	TAC	GCC	CCA	GCT	CTG	CCG	TCC				387
108	Tyr	Leu	Thr	Phe	Leu	Gly	Ala	Pro	Cys	Tyr	Ala	Pro	Ala	Leu	Pro	Ser				
109		-10					-5				1				5					
110																				
111	TGC	AAG	GAG	GAC	GAG	TAC	CCA	GTG	GGC	TCC	GAG	TGC	TGC	CCC	AAG	TGC				435
112	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val	Gly	Ser	Glu	Cys	Cys	Pro	Lys	Cys				
113					10					15					20					
114																				
115	AGT	CCA	GGT	TAT	CGT	GTG	AAG	GAG	GCC	TGC	GGG	GAG	CTG	ACG	GGC	ACA				483
116	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly	Thr				
117				25					30					35						
118																				
119	GTG	TGT	GAA	CCC	TGC	CCT	CCA	GGC	ACC	TAC	ATT	GCC	CAC	CTC	AAT	GGC				531
120	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly				
121			40					45					50							
122																				
123	CTA	AGC	AAG	TGT	CTG	CAG	TGC	CAA	ATG	TGT	GAC	CCA	GCC	ATG	GGC	CTG				579
124	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu				
125		55					60					65								
126																				
127	CGC	GCG	AGC	CGG	AAC	TGC	TCC	AGG	ACA	GAG	AAC	GCC	GTG	TGT	GGT	TGC				627
128	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys				
129		70				75					80				85					
130																				
131	AGC	CCA	GGC	CAC	TTC	TGC	ATC	GTC	CAG	GAC	GGG	GAC	CAC	TGC	GCC	GCG				675
132	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His	Cys	Ala	Ala				
133				90						95					100					
134																				
135	TGC	CGC	GCT	TAC	GCC	ACC	TCC	AGC	CCG	GGC	CAG	AGG	GTG	CAG	AAG	GGA				723
136	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly				
137				105					110					115						
138																				
139	GGC	ACC	GAG	AGT	CAG	GAC	ACC	CTG	TGT	CAG	AAC	TGC	CCC	CCG	GGG	ACC				771
140	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr				
141			120					125					130							
142																				
143	TTC	TCT	CCC	AAT	GGG	ACC	CTG	GAG	GAA	TGT	CAG	CAC	CAG	ACC	AAG	TGC				819
144	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln	His	Gln	Thr	Lys	Cys				
145		135					140					145								
146																				
147	AGC	TGG	CTG	GTG	ACG	AAG	GCC	GGA	GCT	GGG	ACC	AGC	AGC	TCC	CAC	TGG				867
148	Ser	Trp	Leu	Val	Thr	Lys	Ala	Gly	Ala	Gly	Thr	Ser	Ser	Ser	His	Trp				
149		150				155					160					165				
150																				
151	GTA	TGG	TGG	TTT	CTC	TCA	GGG	AGC	CTC	GTC	ATC	GTC	ATT	GTT	TGC	TCC				915
152	Val	Trp	Trp	Phe	Leu	Ser	Gly	Ser	Leu	Val	Ile	Val	Ile	Val	Cys	Ser				

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	170	175	180	
153				
154				
155	ACA GTT GGC CTA ATC ATA TGT GTG AAA AGA AGA AAG CCA AGG GGT GAT			963
156	Thr Val Gly Leu Ile Ile Cys Val Lys Arg Arg Lys Pro Arg Gly Asp			
157	185	190	195	
158				
159	GTA GTC AAG GTG ATC GTC TCC GTC CAG CGG AAA AGA CAG GAG GCA GAA			1011
160	Val Val Lys Val Ile Val Ser Val Gln Arg Lys Arg Gln Glu Ala Glu			
161	200	205	210	
162				
163	GGT GAG GCC ACA GTC ATT GAG GCC CTG CAG GCC CCT CCG GAC GTC ACC			1059
164	Gly Glu Ala Thr Val Ile Glu Ala Leu Gln Ala Pro Pro Asp Val Thr			
165	215	220	225	
166				
167	ACG GTG GCC GTG GAG GAG ACA ATA CCC TCA TTC ACG GGG AGG AGC CCA			1107
168	Thr Val Ala Val Glu Glu Thr Ile Pro Ser Phe Thr Gly Arg Ser Pro			
169	230	235	240	245
170				
171	AAC CAC TGACCCACAG ACTCTGCACC CCGACGCCAG AGATACCTGG AGCGACGGCT			1163
172	Asn His			
173				
174				
175	GAATGAAAGA GGCTGTCCAC CTGGCGGAAC CACCGGAGCC CGGAGGCTTG GGGGCTCCAC			1223
176				
177	CCTGGACTGG CTTCCGTCTC CTCCAGTGGA GGGAGAGGTG GCGCCCCTGC TGGGGTAGAG			1283
178				
179	CTGGGGACGC CACGTGCCAT TCCCATGGGC CAGTGAGGGC CTGGGGCCTC TGTTCGTCTG			1343
180				
181	TGGCCTGAGC TCCCCAGAGT CCTGAGGAGG AGCGCCAGTT GCCCCTCGCT CACAGACCAC			1403
182				
183	ACACCCAGCC CTCCTGGGCC AACCCAGAGG GCCTTCAGAC CCCAGCTGTG TGCGCGTCTG			1463
184				
185	ACTCTTGTGG CCTCAGCAGG ACAGGCCCCG GGCACCTGCCT CACAGCCAAG GCTGGACTGG			1523
186				
187	GTTGGCTGCA GTGTGGTGTT TAGTGGATAC CACATCGGAA GTGATTTTCT AAATTGGATT			1583
188				
189	TGAATTCGGC TCCTGTTTTT TATTTGTCAT GAAACAGTGT ATTTGGGGAG ATGCTGTGGG			1643
190				
191	AGGATGTAAA TATCTTGTTT CTCCTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA			1703
192				
193	A			1704
194				
195				
196	(2) INFORMATION FOR SEQ ID NO:2:			
197				
198	(i) SEQUENCE CHARACTERISTICS:			
199	(A) LENGTH: 283 amino acids			
200	(B) TYPE: amino acid			
201	(D) TOPOLOGY: linear			
202				
203	(ii) MOLECULE TYPE: protein			
204				
205	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			

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206
207 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
208 -36 -35 -30 -25
209
210 Lys Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
211 -20 -15 -10 -5
212
213 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
214 1 5 10
215
216 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
217 15 20 25
218
219 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
220 30 35 40
221
222 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
223 45 50 55 60
224
225 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
226 65 70 75
227
228 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
229 80 85 90
230
231 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
232 95 100 105
233
234 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
235 110 115 120
236
237 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
238 125 130 135 140
239
240 Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
241 145 150 155
242
243 Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
244 160 165 170
245
246 Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
247 175 180 185
248
249 Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
250 190 195 200
251
252 Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
253 205 210 215 220
254
255 Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr
256 225 230 235
257
258 Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/340,690

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